

RESULT 1  
 AAB13956

ID AAB13956 standard; protein; 1402 AA.  
 XX  
 AC AAB13956;  
 XX  
 DT 15-JUN-2007 (revised)  
 DT 16-NOV-2000 (first entry)  
 XX  
 DE Neurospora crassa QDE-1 protein.  
 XX  
 KW Gene silencing; quelling deficient; qde-1; al-1; BOND\_PC;  
 KW RNA-dependent RNA polymerase;  
 KW RNA-dependent RNA polymerase [Neurospora crassa]; GO3968.  
 XX  
 OS Neurospora crassa.  
 XX  
 PN WO200050581-A2.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 16-FEB-2000; 2000WO-IT000048.  
 XX  
 PR 22-FEB-1999; 99IT-RM000117.  
 XX  
 PA (UYRO-) UNIV ROMA LA SAPIENZA.  
 XX  
 PI Macino G, Cogoni C;  
 XX  
 DR WPI; 2000-579171/54.  
 DR N-PSDB; AAA65171.  
 DR PC:NCBI; gi4803727.  
 XX  
 PT Novel polynucleotide encoding a polypeptide which has a silencing activity and comprising a RNA-dependent RNA polymerase domain.  
 XX  
 PS Claim 21; Fig 4; 48pp; English.  
 XX  
 CC The present sequence is the Neurospora crassa QDE-1 protein. This protein has gene silencing activity. The qde-1 gene was isolated by mutational analysis of an al-1 transgenic strain. This strain had an albino phenotype resulting from post-transcriptional silencing of the endogenous al-1 gene. Reversion of this phenotype indicated a mutation in a silencing gene. The silencing gene, qde-1, could then be isolated. Modulation of qde-1 expression may be used to inactivate genes and to silence suppression of genes  
 CC  
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed information from BOND.  
 XX  
 SQ Sequence 1402 AA;

Query Match 100.0%; Score 7397; DB 3; Length 1402;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNPITPRKRNSPVEEIINRLNNNDYNLGLQCVADITLTPHRRKELAESDEDFGRHDKIYRA 60
Db	1 MNPITPRKRNSPVEEIINRLNNNDYNLGLQCVADITLTPHRRKELAESDEDFGRHDKIYRA 60
Qy	61 LNFLYWRKDDSLNQAEANFFIEAKAASSNWVPKAHADPDTLPWSKEPPRAATAGQQWALQ 120
Db	61 LNFLYWRKDDSLNQAEANFFIEAKAASSNWVPKAHADPDTLPWSKEPPRAATAGQQWALQ 120
Qy	121 TVLLEVLRNRFMPPPNNTPGRTFGRTLSGPGLSRPTSTNTKRKDEPANVTFADPPKRSLT 180
Db	121 TVLLEVLRNRFMPPPNNTPGRTFGRTLSGPGLSRPTSTNTKRKDEPANVTFADPPKRSLT 180
Qy	181 RSATGPPIHGAAIPLKFDPDVNTGSKRPSLESENLNQCTKRAKGKLSDNVAAAAPPVPI 240
Db	181 RSATGPPIHGAAIPLKFDPDVNTGSKRPSLESENLNQCTKRAKGKLSDNVAAAAPPVPI 240

Qy 241 ASALDKVPTRRHANTRDPTATGHRRADQVDSFDTSQGTSYGVSSVSACRHNQTTQSSFE 300  
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Db 241 ASALDKVPTRRHANTRDPTATGHRRADQVDSFDTSQGTSYGVSSVSACRHNQTTQSSFE 300  
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Qy 301 APPSQPREKRPVDATVFEAGHLIESPSKGRTTKSHIDNQPLSSSQGETSFSTYYESFPS 360  
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Db 301 APPSQPREKRPVDATVFEAGHLIESPSKGRTTKSHIDNQPLSSSQGETSFSTYYESFPS 360  
|||  
Qy 361 SGGEGAPEPSRSNGLARSEESARSQVQVHAPVVAARLRNIWPKFPKWLHEAPLAVAEV 420  
|||  
Db 361 SGGEGAPEPSRSNGLARSEESARSQVQVHAPVVAARLRNIWPKFPKWLHEAPLAVAEV 420  
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Qy 421 TRLFMHCKVDLEDESLGLKYDPSWSTARDVTDIWKTLYRLDAFRGKPFPEKPPNDVFVTA 480  
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Db 421 TRLFMHCKVDLEDESLGLKYDPSWSTARDVTDIWKTLYRLDAFRGKPFPEKPPNDVFVTA 480  
|||  
Qy 481 MTGNFESKGSAVVLSAVALDYNPDNSPTAPLYLVKLKPLMFEQGCRLTRRGPDFFEIL 540  
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Db 481 MTGNFESKGSAVVLSAVALDYNPDNSPTAPLYLVKLKPLMFEQGCRLTRRGPDFFEIL 540  
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Qy 541 PSPTSTSPSVPPVVKQPGAVEEEVIQWLTMGQHSLVGRQWRAFFAKDAGYRKPLREFQLR 600  
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Db 541 PSPTSTSPSVPPVVKQPGAVEEEVIQWLTMGQHSLVGRQWRAFFAKDAGYRKPLREFQLR 600  
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Qy 601 AEDPKPIIKERVHFFAETGITFRPDVFKTRSVVPAEEPVEQRTEFKVSQMLDWLLQLDNN 660  
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Db 601 AEDPKPIIKERVHFFAETGITFRPDVFKTRSVVPAEEPVEQRTEFKVSQMLDWLLQLDNN 660  
|||  
Qy 661 TWQPHLKLF SRIQLGLSKTYAIMTLEPHQIRHHKTDLSPSGTGEVMNDGVGRMSRSVAK 720  
|||  
Db 661 TWQPHLKLF SRIQLGLSKTYAIMTLEPHQIRHHKTDLSPSGTGEVMNDGVGRMSRSVAK 720  
|||  
Qy 721 RIRDVLGLGDVPSAVQGRFGSAKGMWVIDVDDTGDEDWIETYPSQRKWECDFVDKHQRTL 780  
|||  
Db 721 RIRDVLGLGDVPSAVQGRFGSAKGMWVIDVDDTGDEDWIETYPSQRKWECDFVDKHQRTL 780  
|||  
Qy 781 EVRSVASELK SAGLNQLLPVLED RARDKV KMRQAIGDRLINDLQRQFSEQKH ALNRPVE 840  
|||  
Db 781 EVRSVASELK SAGLNQLLPVLED RARDKV KMRQAIGDRLINDLQRQFSEQKH ALNRPVE 840  
|||  
Qy 841 FRQWVYESYSSRATRVSHGRVPFLAGLPDSQEETLNFLMN SGFDPKKQKYLQDIAWDLQK 900  
|||  
Db 841 FRQWVYESYSSRATRVSHGRVPFLAGLPDSQEETLNFLMN SGFDPKKQKYLQDIAWDLQK 900  
|||  
Qy 901 RKCDTLKSKLNIRVGRSAYIYMIADFVGVL ENEVHVGFS SKFRDEEESFTLLSDCDVLV 960  
|||  
Db 901 RKCDTLKSKLNIRVGRSAYIYMIADFVGVL ENEVHVGFS SKFRDEEESFTLLSDCDVLV 960  
|||  
Qy 961 ARSPAHP PSDIQRVRAVFKPELHS LKDVIIFSTKGDVPLAKKL SGGDYDG DMAWVCWDPE 1020  
|||  
Db 961 ARSPAHP PSDIQRVRAVFKPELHS LKDVIIFSTKGDVPLAKKL SGGDYDG DMAWVCWDPE 1020  
|||  
Qy 1021 IVDGFVN AEMPLEP DLSR YLKKD KTFK QLMA SHGT GSAA KEQT TYDMI QK SFH FAL QPN 1080  
|||  
Db 1021 IVDGFVN AEMPLEP DLSR YLKKD KTFK QLMA SHGT GSAA KEQT TYDMI QK SFH FAL QPN 1080  
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Qy 1081 FLGMCTNYKERLCYINNSVS NKP AI ILSS LVGNL DVQSKQ GIVF NEASWA QL RRELLGGA 1140  
|||  
Db 1081 FLGMCTNYKERLCYINNSVS NKP AI ILSS LVGNL DVQSKQ GIVF NEASWA QL RRELLGGA 1140  
|||  
Qy 1141 LSLPDP MYKSDS WLGR GEPT H IDYLKF SIAR PAID KE LEAF HN AMKA AK DT EDGA HFWD 1200  
|||  
Db 1141 LSLPDP MYKSDS WLGR GEPT H IDYLKF SIAR PAID KE LEAF HN AMKA AK DT EDGA HFWD 1200  
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Qy 1201 PDLAS YYT FFKEISDKS R S ALLFT TLKN RIGE VEKEY GRL VKN KEMR DS KDPY PV RVNQ 1260  
|||  
Db 1201 PDLAS YYT FFKEISDKS R S ALLFT TLKN RIGE VEKEY GRL VKN KEMR DS KDPY PV RVNQ 1260  
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Qy 1261 VYE KWCAIT PEAMDKSG ANYD SKVIR LLELSFLAD REMNT WALL RASTA FK LY HKSPKF 1320  
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Db 1261 VYEKWCAITPEAMDKGANYDSKVIRLLELSFLADREMNTWALLRASTAFKLYYHKSPKF 1320  
Qy 1321 VWQMAGRQLAYIKAQMITSRPGEGAPALMTAFMYAGLMPDKFTKQYVARLEGDGSEYPDP 1380  
Db 1321 VWQMAGRQLAYIKAQMITSRPGEGAPALMTAFMYAGLMPDKFTKQYVARLEGDGSEYPDP 1380  
Qy 1381 EVYEVLGDDDFDGIGFTGNGDY 1402  
Db 1381 EVYEVLGDDDFDGIGFTGNGDY 1402